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LOCUS      ATH243015              5000 bp      DNA      linear      PLN 01-JUN-2001
DEFINITION Arabidopsis thaliana LGT1 gene, and partial FUSCA6 gene.
ACCESSION  AJ243015
VERSION    AJ243015.1   GI:7799776
KEYWORDS   FUSCA6 gene; FUSCA6 protein; LGT1 gene; like glycosyl transferase
1.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosid; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1
AUTHORS    Tavares,R., Aubourg,S., Lecharny,A. and Kreis,M.
TITLE      Organization and structural evolution of four multigene families in
            Arabidopsis thaliana: AtLCAD, AtLGT, AtMYST and AtHD-GL2
JOURNAL    Plant Mol. Biol. 42 (5), 703-717 (2000)
PUBMED     10809443
REFERENCE  2 (bases 1 to 5000)
AUTHORS    Tavares,R.
TITLE      Direct Submission
JOURNAL    Submitted (07-MAY-1999) R. Tavares, Institut de Biotechnologie des
            Plantes, Biologie du Developpement des Plantes, Universite
            Paris-Sud, Batiment 630, F-91405 Orsay Cedex, FRANCE
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ORIGIN

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Best Local Similarity:	64.5%	Mismatches:	3
Query Match:	90.5%	Indels:	369
DB:	4	Gaps:	9

US-10-544-180A-2 (1-673) x ATH243015 (1-5000)

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Qy      50 ----- 50
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Qy	159	-----GlnLeuArgGluLysArgArgGluMetArgAlaAsnGluLeuValGln	174
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Qy	175	HisAsnAspAspThrIleLeuLysLeuGluAsnAlaAlaIleGluArgSerLysSerVal	194
Db	1948	CACAATGATGACACGATTTTGAAACTCGAAAAGTCCATTGAACGCTCTAAGTCTGTT	2007

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Db	2068	GATTCAAAATATACGCTTGATGCGGGATCAAGTAATAATGGCTAGAGTCTATAGTGGGATT	2127
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Qy	324	AlaAlaLysThrIleProAsnProIleHisCysLeuSerMetArgLeuThrIleAspTyr	343
Db	2488	GCAGCAAAACCATTCCAAATCCTATCCATTGCCTATCAATGCGCTTGACTATCGATTAC	2547
Qy	344	TyrLeuLeuSerProGluLysArgLysPheProArgSerGluAsnLeuGluAsnProAsn	363
Db	2548	TATCTTCTGTCTCCGGAGAAAAGAAAATTCCTCGGAGTGAAAACCTAGAAAACCTAAT	2607
Qy	364	LeuTyrHisTyrAlaLeuPheSerAspAsnValLeuAlaAlaSerValValValAsnSer	383
Db	2608	CTTTATCATTATGCCCTCTTTTCCGACAAATGATTAGCTGCATCAGTAGTTGTTAACTCA	2667
Qy	384	ThrIleMetAsnAlaLys-----	389
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Db	2727	TGTATGTTTAATTTTAGATACGATTGCAGAGCTGAAATTAATAATGTCTTTATTCCCTA	2786
Qy	390	-----AspProSerLysHisValPheHisLeuValThrAspLysLeuAsnPheGly	406
Db	2787	TATGTGCAGGATCCTTCTAAGCATGTTTTTCACCTGTGCACGGATAAATCAATTCGGA	2846
Qy	407	AlaMetAsnMetTrpPheLeuLeuAsnProProGlyLysAlaThrIleHisValGluAsn	426
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